regions of the preceding sequences corresponding to a shifting frame greater than or equal to 14 nucleotides or their complementary sequences.

4. (Amended) Transcripts, characterized in that they are generated from the sequences as claimed in [any one of claims 1 to 3] claim 1.

5. (Amended) A diagnostic reagent for the differential detection if complete or partial human endogenous nucleic sequences, having retroviral motifs, selected from the sequences SEQ ID NO: 1 and/or SEQ ID NO: 2, characterized in that it is selected from the group consisting of the sequences SEQ ID NO: 1-22, 28, 37-57, 59-61 and 121-122, the complementary nucleic sequences and the reverse sequences complementary to the preceding sequences, of nucleotide fragments capable of defining or of identifying the sequences SEQ ID NO: 1 and/or SEQ ID NO: 2 and any flanking sequence or any sequence overlapping them as well as of fragments derived from the coding regions of the sequences SEQ ID NO: 1-22 and 61, corresponding to a shifting frame greater than or equal to 14 nucleotides or their complementary sequences, optionally labeled with an appropriate label.

10. (Amended) A method for the rapid and differential detection of the endogenous retroviral nucleic sequences of the *env* or *env* and *gag* type, their normal or pathological variants, by hybridization and/or gene amplification, carried out using a biological sample, which method is characterized in that it comprises:

(a) a step in which a biological sample to be analyzed is brought into contact with at least one probe as claimed in claim 5[, claim 6 or claim 8,] and

(b) a step in which the product(s) resulting from the nucleotide sequence-probe interaction is detected by any appropriate means.

11. (Amended) The method of detection as claimed in claim 10, characterized in that it comprises:

- prior to step (a):

- a step of preparing the relevant biological tissue or fluid,

- a step of extracting the nucleic acid to be detected, and

- at least one gene amplification cycle carried out with the aid of at least one reagent [as claimed in any one of claims 5 to 7] selected from the group consisting of the sequences SEQ ID NO: 1-22, 28, 37-57, 59-61 and 121-122, the complementary nucleic sequences and the reverse sequences complementary to the preceding sequences, of nucleotide fragments capable of defining or of identifying the sequences SEQ ID NO: 1 and/or SEQ ID NO: 2 and any flanking sequence or any sequence overlapping them as well as of fragments derived from the coding regions of the sequences SEQ ID NO: 1-22 and 61, corresponding to a shifting frame greater than or equal to 14 nucleotides or their complementary sequences, optionally labeled with an appropriate label, and subsequent to step (b):

- a step of comparing the nucleic sequences obtained in the said biological sample with the human endogenous retroviral sequences SEQ ID NO: 1 or SEQ ID NO:2 or to a sequence exhibiting a level of homology with SEQ ID NO: 1 or SEQ ID NO:2 greater than or equal to 80% on more than 190 nucleotides or greater than or equal to 70% on more than 600 nucleotides for the *env*-type domains [as claimed in any one of claims 1 to 3], by any appropriate means and in particular by sequencing, Southern blotting, restriction cleavage, SSCP or any other method which makes it possible to identify an insertion or a deletion or a single mutation between the various sequences compared.

12. (Amended) A method of detecting the transcripts as claimed in claim 4, characterized in that it comprises:

- collecting messenger RNAs obtained from control biological samples and from a similar sample collected from patients, and

- the qualitative and/or quantitative analysis of the said mRNAs by *in situ* hybridization, by dot-blot, Northern blotting, RNAse mapping or RT-PCR, with the aid of a diagnostic reagent selected from the group consisting of the sequences SEQ ID NO: 1-22, 28, 37-57, 59-61 and 121-122, the complementary nucleic sequences and the reverse sequences complementary to the preceding sequences, of nucleotide fragments capable of defining or of identifying the sequences SEQ ID NO: 1 and/or SEQ ID NO: 2 and any flanking sequence or any sequence overlapping them as well as of fragments derived from the coding regions of the sequences SEQ ID NO: 1-22 and 61, corresponding to a shifting frame greater than or equal to 14 nucleotides or their complementary sequences, optionally labeled with an appropriate label [as claimed in any one of claims 5 to 9].

13. (Amended) Chimeric sequences, characterized in that they consist of a fragment of 17 to 40 nucleotides of a flanking sequence selected from the group consisting of transcripts and cDNAs of the genomic sequences, which encode all or part of a factor, whose function, regulation/deregulation or alteration is associated with the normal or pathological expression or with the regulation/deregulation of motifs belonging to said HERV-7q family, these sequences corresponding to nucleotide sequences encoding genes situated in flanking regions situated upstream and/or downstream of a retroviral sequence of the said HERV-7q family and in which one of the ends cannot be at a distance exceeding 120 kb, associated with an endogenous retroviral motif of the HERV-7q type comprising between 17 and 40 nucleotides as claimed in [claims 1 to 4] claim 1.

14. (Amended) A method for the detection and/or evaluation of an overexpression/underexpression or of a modification of at least one of the endogenous retroviral sequences or fragments of sequences of the HERV-7q type and/or of their associated flanking sequences, wherein the sequence are SEQ ID NO: 1 or SEQ ID NO:2 or

to a sequence exhibiting a level of homology with SEQ ID NO: 1 or SEQ ID NO:2 greater than or equal to 80% on more than 190 nucleotides or greater than or equal to 70% on more than 600 nucleotides for the *env*-type domains [as claimed in any one of claims 1 to 9], characterized in that it comprises:

- depositing on an appropriate support, cDNA obtained from clones, PCR products obtained from genomic DNA, RT-PCR products obtained from transcripts or from specific oligonucleotide sequences, the said DNA sequences being endogenous retroviral sequences or fragments of sequences of the HERV-7q type and/or their flanking sequences, consisting of transcripts and cDNAs of the genomic sequences, which encode all or part of a factor, whose function, regulation/deregulation or alteration is associated with the normal or pathological expression or with the regulation/ deregulation of motifs belonging to the said HERV-7q family, these sequences corresponding to nucleotide sequences encoding genes situated in flanking regions situated upstream and/or downstream of a retroviral sequence of the said HERV-7q family and in which one of the ends cannot be at a distance exceeding 120 kb, and/or a chimeric sequence as claimed in claim 13,

- the hybridization of the said support with at least one appropriately labeled probe obtained, for example, by retrotransposition of an RNA mixture obtained from biological cells, tissues or fluids obtained from controls reputed to be normal, from members of various ethnic populations, from patients suffering from pathological conditions often associated with expression of retroviruses, such as tumor processes, or such as autoimmune diseases, and

- the detection of the hybrids formed.

16. (Amended) The method as claimed in claim 14 [or claim 15], characterized in that the said support comprises, in addition, any endogenous or exogenous retroviral sequence.

17. (Amended) The kit for the detection and/or evaluation of an autoimmune disease and in particular of neuropathological conditions with an autoimmune etiology, characterized in that it comprises, in addition to the buffers necessary for carrying out a method according to [any one of claims 14 to 16] claim 14:

- diagnostic reagents A selected from the sequences SEQ ID NO: 1 and/or SEQ ID NO: 2, characterized in that it is selected from the group consisting of the sequences SEQ ID NO: 1-22, 28, 37-57, 59-61 and 121-122, the complementary nucleic sequences and the reverse sequences complementary to the preceding sequences, of nucleotide fragments capable of defining or of identifying the sequences SEQ ID NO: 1 and/or SEQ ID NO: 2 and any flanking sequence or any sequence overlapping them as well as of fragments derived from the coding regions of the sequences SEQ ID NO: 1-22 and 61, corresponding to a shifting frame greater than or equal to 14 nucleotides or their complementary sequences, optionally labeled with an appropriate label [as claimed in any one of claims 5 to 9], and

- reagents B consisting of the transcripts and cDNAs of the genomic sequences, which encode all or part of a factor, whose function, regulation/deregulation or alteration is associated with the normal or pathological expression or with the regulation/deregulation of motifs belonging to said HERV-7q family, these sequences corresponding to nucleotide sequences encoding genes situated in flanking regions situated upstream and/or downstream of a retroviral sequence of said HERV-7q family, of which one of the ends cannot be at a distance exceeding 120 kb,

- which reagents are preferably attached to an appropriate support.

19. (Amended) Translational products, characterized in that they are encoded by a nucleotide sequence as claimed in [any one of claims 1 to 4] claim 1.

20. (Amended) A peptide, characterized in that it is capable of being expressed with the aid of a nucleotide sequence selected from the group consisting of the sequences SEQ ID NO: 1-22, 28 and 61 as claimed in [any one of claims 1 to 4] claim 1.

22. (Amended) The peptide as claimed in claim 20 [or claim 21], characterized in that it is selected from the group consisting of:

- the sequences SEQ ID NO: 23-36;

- the sequence SEQ ID NO: 58;

- a C-terminal fragment of the sequence SEQ ID NO: 26, either from the amino acid 291, or from the amino acid 321, starting from the first methionine of the sequence SEQ ID NO: 26;

- a peptide of the CKS-17/CKS-25 type present in one of the sequences SEQ ID NO: 23-36 or 58; and

- the peptides having affinity with one of the haplotypes of the class I or class II HLA system and in particular the fragments 399-411, 244-271 of enverin, as well as the peptides having the sequence SEQ ID NO: 68-118, in accordance with Table I.

23. (Amended) The peptide as claimed in [any one of claims 20 to 22] claim 20, characterized in that it is obtained from nucleic sequences as claimed in any one of claims 1 to 4, in which at least one non-sense codon may be replaced with a codon encoding one of the following amino acids: Phe (F), Leu (L), Ser (S), Tyr (Y), Cys (C), Trp (W), Gln (Q), Arg (R), Lys (K), Glu (E) or Gly (G).

26. (Amended) The composition as claimed in claim 24 [or claim 25], characterized in that said peptide has the sequence SEQ ID NO: 120.

27. (Amended) An antibody, characterized in that it is directed against one or more of the peptides as claimed in [any one of claims 20 to 23] claim 20.

30. (Amended) A method for the identification and detection of endogenous retroviral motifs which are abnormally expressed in the context of pathological conditions associated with cancer, or of neuropathological conditions, in particular autoimmune neuropathological conditions, at the forefront of which is multiple sclerosis, characterized in that it comprises the comparative analysis of the sequences extracted from a biological sample and the sequences as claimed in [any one of claims 19 to 23] claim 19.

31. (Amended) An application of the sequences as claimed in [any one of claims 1 to 9, 13, 14 or 19 to 23] claim 1 to the diagnosis of, to the prognosis of, to the evaluation of genetic susceptibility to, any induced, congenital or acquired human diseases, in particular those with cancerous, autoimmune and/or neurological components, such as multiple sclerosis, the associated syndromes and the neurodegenerative diseases in which all or part of the sequences [as claimed in to any one of claims 1 to 5] in claim 1 and related endogenous or exogenous forms are involved.

32. (Amended) Hybrid nucleic sequences, characterized in that they comprise sequences or motifs as claimed in [any one of claims 1 to 9] claim 1, combined with sequences or motifs of endogenous origin or of exogenous origin or induced exogenously.

33. (Amended) A recombinant cloning or expression vector, characterized in that it comprises a nucleic sequence as claimed in [any one of claims 1 to 4] claim 1.

35. (Amended) A gene therapy vector, characterized in that it comprises all or part of the endogenous retroviral nucleic sequences of the HERV- 7q type as claimed in [any one of claims 1 to 4] claim 1.--